

1 **Interdependence of linkage disequilibrium, chromatin architecture and compositional**
2 **genome organization of mammals**

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4 **Running title: A common ground for meiotic and mitotic chromatin folding in**
5 **mammals**

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ABSTRACT

14 Analysing chromatin architecture in interphase nuclei and recombination maps of human
15 and mouse, we observed that blocks of elevated linkage disequilibrium tends to coincide with
16 topologically associated domains (TADs) and isochores. There is a strong correlation between
17 the GC level of TADs, double strand break (DSB) frequency and the local recombination rate.
18 In particular, cold and hot spots of recombination tend to fall in AT- and GC-rich TADs,
19 respectively. Also, binding of proteins which are critical for meiotic recombination hot spots
20 (PRMD9, Spo11, DMC1 and H3K4me3) is positively correlated with the GC level of TADs.
21 We conclude that the occurrence of meiotic DSB and recombination is associated with the
22 same (com)positional features that constrain the architecture of chromosomes in the
23 interphase nucleus of progenitor germ cells or pre-leptotene spermatocytes. This raises the
24 possibility that regional variation of recombination is defined by compositional and epigenetic
25 factors underlying chromatin architecture.

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27 Key words: Recombination frequency, meiosis, chromatin loop, DNA sequence, epigenetic
28 program.

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INTRODUCTION

30 A relationship between genome organization and recombination was discovered from
31 banding of human chromosomes several decades ago. It was shown that translocations are not
32 randomly located on chromosomes and that R bands and G/R borders were the sites of DNA
33 exchanges and included the “hot spots” of mitotic chiasmata (Hecht 1988; Kuhn and Therman
34 1986). These observations suggested an association with compositional discontinuities
35 (change of GC % along chromosomes) (Bernardi 1989; Ikemura and Wada 1991; Holmquist,
36 1992), which was later reported (Eyre-Walker 1993a) to be statistically significant. It was
37 proposed that active chromosome domains could be more accessible to the base-mismatch
38 repair system, investigated by Brown and Jiricny (1987, 1988), which preferentially changes
39 mismatched A's and T's into G's and C's. Such mismatch repair, acting during recombination
40 and recognized as gene conversion, would drive recombinogenic domains to GC richness.
41 GC-biased repair of gene conversion (BGC) was suggested as the most likely explanation
42 (Holmquist 1992; Eyre-Walker 1993b). With accumulating data from the human genome
43 project, local rates of recombination were later shown to be positively correlated with regional
44 GC levels in the human genome (Fullerton *et al.* 2001). Regions of weak and strong linkage
45 disequilibrium (LD) were found to be remarkably consistent across human populations
46 suggesting that GC%, DNA polymorphism and repeat content are strongly associated with the
47 local extent of LD, where regions of strong LD are typically GC-poor (Smith *et al.* 2005).
48 BGC is considered by some authors to be the inducer of the correlations between local GC %
49 (isochores) and recombination rate (Duret and Galtier 2009; Weber *et al.* 2014). Other authors
50 argue that local GC-richness may be the driving force for recombination (Marsolier-Kergoat
51 *et al.* 2009). Whole genome sequencing of tetrad products from *Saccharomyces*, *Neurospora*,
52 *chlamydomonas* and *Arabidopsis* did not show GC-bias, implying that a GC% vs.
53 recombination correlation is unlikely to be explained by gene conversion (Liu *et al.* 2018).

54 It was shown (Blat *et al.* 2002) that meiotic chromosomal protein loading is modulated by
55 isochores and that R-bands (GC-rich isochores dense regions) differentially favor double-
56 strand break (DSB) formation during meiosis. In mice and humans, spermatocytes begin to
57 enter leptotene, the first stage of meiotic prophase and later in this stage chromosomes are
58 organized in alternating domains of greater and lower DSB activity (Lichten and de Massy
59 2011; Grey *et al.* 2011; Grey *et al.* 2017). But features that influence DSB activity at the scale
60 of chromosomal domains, such as chromatin loops (also called contact domains), are still
61 poorly known. It is widely accepted that the binding of transcription factors and chromatin
62 modifiers influences DSB density (Lichten 2008) and that DSBs occur in regions of
63 accessible chromatin that are present in mitotic as well as in meiotic cells. Along with meiotic
64 DSB repair, the search for homology and the catalysis of strand exchange are likely to be
65 spatially and temporally coordinated to allow for the build-up of higher order chromosome
66 structures (for example, synaptonemal complex, chromosome axes and chromatin loops); this
67 is required for the recombination event to successfully join homologues (Zikler and Kleckner
68 1999; Neal and Keeney 2006; Kleckner 2006). Cohesin has an architectural role in the
69 organization of interphase chromosomes and similar roles have been proposed for cohesin and
70 the related condensin complexes in meiotic and mitotic chromosomes (Tedeschi *et al.* 2013;
71 Ono *et al.* 2003).

72 The entry of pre-leptotene spermatocytes (PLS) into meiosis is accompanied by several
73 epigenetic changes, in primates as well as in mice. The location of most DSBs is correlated
74 with the trimethylation of histone 3 lysine 4 (H3K4me3) by the DNA binding enzyme
75 PRDM9 (Hayashi *et al.* 2005; Baudat *et al.* 2010; Brick *et al.* 2012). In mouse, 200 DSBs
76 occur per meiosis, of which 15 to 35 will lead to crossovers (COs), and the remainder to non-
77 crossovers (NCO) products (Handel and Schimenti 2010), indicating an excess of DSB
78 events. These additional DSBs serve as facilitators of the process of homology searching and
79 pairing but must be repaired as precisely as those designated to become crossovers (Gray and

80 Cohen 2016). The outcome is a heterogeneous recombination chromosomal profile where
81 recombination is suppressed in specific mega-base sized regions (Smagulova et al., 2011).

82 To gain a comprehensive large scale view on the recombination chromatin landscape and
83 dynamic, accumulated large numbers of CO events between the founder haplotypes over
84 successive generations, and high density genotyping or genome-wide sequencing, can be used
85 to obtain accurate localization of these events in human and mouse. The recombination map
86 of accumulated CO events in mice (Margot et al. 2017) and LD-blocks from human
87 population are put together to address questions regarding the link between recombination and
88 chromatin architecture, in particular Topologically Associated Domains (TADs) (Dixon et al.
89 2012).

90 Lately LD-blocks and TADs have also been investigated in two other studies which were
91 deposited on bioRxiv. The first study (Greber et al. 2018) did not find a significant correlation
92 of TAD boundaries with classical LD blocks, but when applying a new measure, called
93 "Linkage Probability", the authors could report a strong association. The second article
94 (Whalen and Pollard 2018) denies the existence of such an association.

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MATERIAL AND METHODS

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Recombination and LD-blocks data sets

98 Multiparent populations such as the Diversity Outbred (DO) mouse stock represents a
99 valuable resource of large numbers of crossover events accumulated in present day sibs from
100 founder haplotypes. It thus allows for an exhaustive exploration of the recombination
101 landscape. We used the data from Morgan et al. 2017, a high-density genotype data set from
102 6886 DO (diversity Outbred) mice spanning 16 breeding generations, in which 2.2 million CO
103 events were localized in intervals with a median size of 28 kb. The construction of linkage
104 maps in pedigrees assumes that every CO is distinct, and can be attributed to one of two
105 specific meioses (in the case of unknown phase). By excluding shared by descent COs, the

106 authors reduced the total dataset of 2.2 million COs to a set of distinct COs (n=749,560).
107 Coordinates and haplotypes of distinct COs as well as cold spots location are obtained from
108 Morgan *et al.* 2017.

109 Linkage disequilibrium blocks in human populations are based on the classical r^2 metric
110 used to estimate if a genetic variant is in LD with another genetic variant (Pritchard and
111 Przeworski 2001; Hill and Robertson 1968). LD is defined as the nonrandom association of
112 alleles (of a given gene for example) at distinct close by loci. For our purpose, we used LD-
113 blocks identified with a recently published method (Berisa and Pickrell 2016) applied to
114 sequencing data from European (CEU, TSI, GBR, FIN and IBS), African (YRI, LWK and
115 ASW) and East Asian (CHB, JPT and CHS) populations in the 1000 Genomes Phase 1 dataset
116 (Auton *et al.* 2015). Covariance matrix was separately computed in the European, East Asian,
117 and African meta-populations. The mean block size of 10 000 SNPs is set and used by the
118 algorithm to define the block boundaries. To define human LD-blocks from 1000 genomes
119 dataset, two sets of SNPs are defined as ‘approximately independent’ if the pair wise r^2
120 between SNPs in different sets is close to zero. This led to 2605, 1467 and 1725 LD-blocks in
121 African, East Asian and European, respectively. The human recombination map
122 (HapmapII_GRCh37_RecombinationHotspots) was downloaded from the ftp site of the 1000
123 genome project.

124 **TAD data sets**

125 To study the correlation between chromatin structure and recombination frequency in
126 mammalian cells, we used TAD coordinates from the genome-wide chromatin interaction
127 frequencies (Hi-C experiments) performed on human and mouse embryonic stem cells
128 (Dixon *et al.* 2012). We used the UCSC batch coordinate conversion (liftOver at
129 <http://genome.ucsc.edu/cgi-bin/hgLiftOver>) to convert isochore coordinates reported by
130 Costantini *et al.* 2006 from hg18 to hg19 and mouse genome assembly mm9 to mm10 for
131 compatibility with recombination hot/cold spot coordinates. Mouse isochore maps were

132 visualized with "draw-chromosome-gc.pl" (Paces *et al.* 2004) and Hi-C maps using
133 Juicebox (Durand *et al.* 2016). We also made use of the recently published (Jung *et al.*
134 2017) Hi-C data from mouse sperm, GEO accession: GSE79230 and mouse embryonic
135 stem cells (Bonev *et al.* 2017), GEO accession: GSE96107.

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137 **ChIP-Seq and sequencing data**

138 Meiotic DSBs are induced by dimers of the conserved topoisomerase-like protein Spo11
139 via a transesterase reaction that links a Spo11 molecule to each 5' end of the broken DNA and
140 release of covalently bound Spo11 to short oligonucleotides (Spo11 oligos). Mapping Spo11
141 oligos data of mouse spermatocytes are obtained from Lange *et al.* 2016, a total of 13.960
142 DSB hotspots were defined as regions where the SPO11-oligo is mapping. Genomic
143 coordinates of the strand-exchange protein DMC1-bound single strand DNA from
144 spermatocytes, H3K4me3 and the DNA-binding site of the zinc finger, histone
145 methyltransferase PRDM9 were obtained from Lange *et al.* 2016 and Grey *et al.* 2017.

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147 **Statistical analysis**

148 We asked whether the TADs, isochores and LD-blocks overlap more than expected by
149 chance. As a quantitative assessment, we performed an association analysis of genomic
150 regions based on permutation tests using the R/Bioconductor package regioneR (Gel *et al.*
151 2016). The outcomes of the permutation were subsequently evaluated with the p-values and
152 z-scores of the test. When performing an association analysis, it is possible to detect
153 associations that are not reflective of boundary proximity, although they may be statistically
154 significant. With the "local z-score" function (Gel *et al.* 2016) one can test whether the
155 association between TADs or isochores and LD-blocks is specifically due to the common
156 boundary positions of the analyzed regions. The main function to perform a permutation test

157 with regioneR is “*permTest*”, which takes a region set (RS), a randomization function and an
158 evaluation function as input and returns the object “*permTestResults*” with the computed
159 p-value and z-score which is calculated iteratively with shifted positions in the RS input set.
160 We calculate z-scores for shifts of 500 kb in 5' and the 3' direction from an original position,
161 the focal site. Plotting average z-scores versus shifted positions, one can observe how the
162 value of the z-score changes when moving away from the focal site: a sharp peak at the centre
163 indicates that the association is highly dependent on the specific genomic coordinates while a
164 flat profile indicates regional or diffuse association.

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RESULTS

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Recombination rate and TADs GC % are strongly correlated

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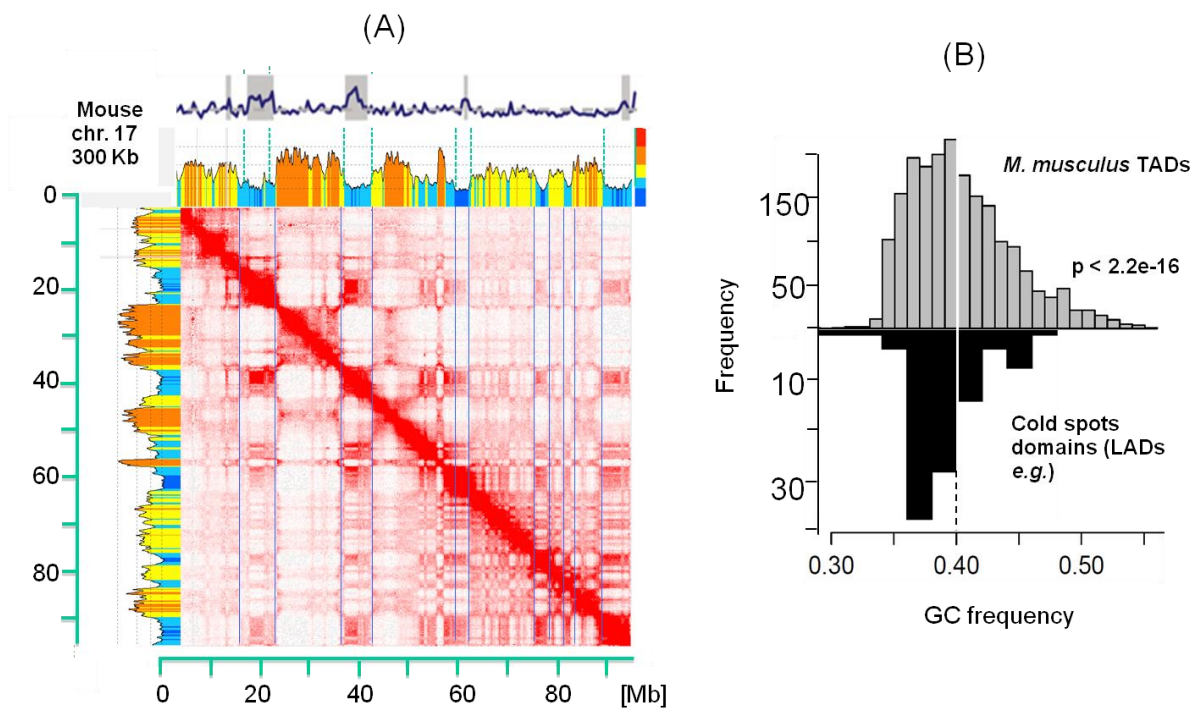
181

It is known that recombination rates and GC% are positively correlated in the human genome (Fullerton *et al.* 2001), as had been suspected from early chromatin and molecular studies (see Introduction). Here, we revisit this relationship in the light of chromatin TAD organization and density of DSB sites. At the time of DSB formation, most DSBs occur in loop sequences (Blat *et al.* 2002). Hence, the DSB distribution could be affected by loop size (Grey *et al.* 2017; Wang *et al.* 2017) and composition.

To test for a potential relation between TADs and the recombination map, we used the Hi-C map constructed from round spermatids (Jung *et al.* 2017) and a map of recombination cold spots constructed from a DO mice cohort (Morgan *et al.* 2017). As expected (Jung *et al.* 2017), similar results are obtained with embryonic stem (ES) cells (Bonev *et al.* 2017) (Figure S1). As an illustrative example, Figure 1a shows the co-mapping of cold spot domains, isochores and chromatin domains from mouse chromosome 17. Recombination cold spots tend to fall into GC-poor chromosomal domains, which are also frequently found to be attached to the interphase lamina, the “Lamina Associated Domains” (LADs) (Meuleman *et*

182 *al.* 2013; Kind *et al.* 2015; Jabbari and Bernardi, 2017). This observation is not limited to
183 mouse chromosome 17. A histogram of GC% of cold spots containing TADs from all
184 chromosomes (Figure 1b) shows that the paucity of cold spot in GC-rich TADs is a general
185 feature (p-value < 2.2e-16).

Figure 1



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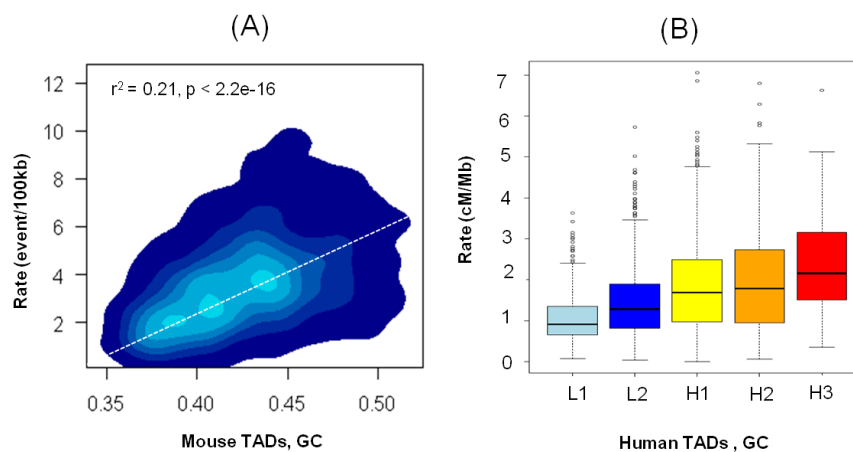
187 **Figure 1. Spatial correlation between recombination rate, TADs/LADs and isochores.**

188 (A) The heat map of chromatin interactions in mouse chromosome 17 (from Jung *et al.*
189 2017) is aligned to the recombination profile from Morgan *et al.* and to the corresponding
190 compositional profile drawn from mm10 genome assembly, using a sliding window of 300
191 Kb. Increasing GC levels are represented in different colours, deep blue, light blue, yellow,
192 orange and red, respectively; the multi-coloured vertical bars on the top right indicate GC
193 levels that correspond to the compositional boundaries among isochores families. Blue line
194 delimits GC-poor isochores and broken black lines indicate cold spots (in grey), very
195 similar results are obtained with ES cells Hi-C interaction matrices (Figure S1). (B) GC

196 histogram of embryonic stem cells TADs from Dixon *et al.* (top) and cold spots intervals
197 (bottom) defined in Morgan *et al.* 2017.

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199 In agreement with the results of figure 1a and 1b, we observe a significant positive correlation
200 between recombination rate and TAD GC% in DO mouse (Figure 2a). The same trend is
201 observed for human, where it is possible to draw a box-plot since isochore boundaries are
202 well defined in this case (Costantini *et al.* 2006; Jabbari and Bernardi, 2017) (Figure 2b).



203

204 **Figure 2. Positive correlation between recombination rate and isochore or GC level of**
205 **TADs.** (A) Contour plot representing the correlation between TADs GC level and
206 recombination rate based on data from Morgan *et al.* 2017. (B) Box plot representing
207 TADs GC level correlation with recombination of human using 1000 genome data. L1, L2,
208 H1, H2 and H3 correspond isochore families (for more details see Jabbari and Bernardi
209 2017).

210

211 Judging from the human and mouse analysis, we hypothesize that the correlation between
212 recombination rate, local chromatin architecture and GC% is a general property of
213 mammalian genomes. Binding events of key recombination proteins mapped around DSB

214 sites are also positively correlated with each other, with recombination rate and with TADs
215 GC % (Table 1).

216 **Table 1: Correlations between genomic features.** R is recombination event per 100 Kb;
217 blue and black respectively refer to RJ2 and B6 mouse strain data from Grey *et al.* 2017; red
218 refers to data from Lange *et al.* 2016 on B6 mouse strain. All *p*-values are $< 2 \cdot 2e-16$ except
219 for spo11 vs. Prdm9 ($r = 0.16, p = 3.31e-13$).

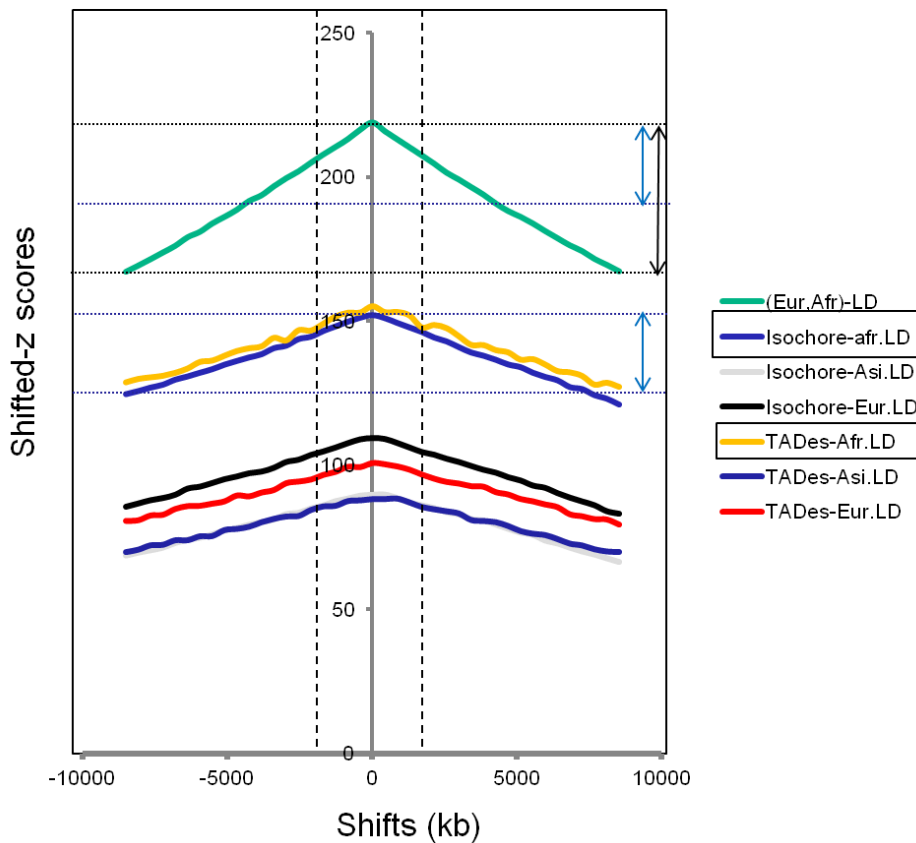
	TADs GC	R	Spo11	Prdm9	H3K4me3	DMC1
TADs GC		0.46	0.38	0.25-0.32	0.35-0.43	0.26-0.20
R			0.38	0.34-0.39	0.22-0.38	0.33
Spo11				0.86	0.24-0.20	0.49-0.21
Prdm9					0.40-0.55	0.21-0.14
H3K4me3						0.61-0.41

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222 Linkage disequilibrium blocks match TADs and LADs

223 The boundaries of recombination cold spots and TAD domains appear to overlap, as
224 visualized in the coarse-scale heat map shown in Figure 1a. To corroborate this visual
225 evidence quantitatively we tested for boundary overlap between blocks of linkage
226 disequilibrium (LD), TADs, and isochores using data from human 1000 genomes project. The
227 statistical tests for overlap between TADs or isochores and LD-blocks are all significant
228 (Figure S2). There is indeed a clear non-random association (all *p*-values are = 0.001)
229 between the two sets of genomic intervals (isochores or TADs and LD-blocks). Because
230 overlap does not mean boundary proximity, we analyzed the overlap of genomic ranges
231 taking into account boundary matches. To assess the strength of boundary sharing between
232 LD and TAD blocks, as a reference, we first determined the boundary sharing z-score profile
233 for LD blocks of European and African human populations (Figure 3).



234

235 **Figure 3. TADs, Isochores and LD-blocks boundaries concordance.** Shifted z-score
236 (on the y-axis) changes when moving the RS interval (x-axis): the peak at the centre
237 indicates that the association is dependent on the genomic coordinates, while a flat profile
238 will indicate that the association is regional. Abbreviations: asi. LD, afr. LD and eur. LD
239 correspond to Asian, African and European linkage disequilibrium blocks, respectively.
240 Black and blue arrows show the difference in drop of z-scores between afr.LD vs. eur.LD
241 and isochores or TADs vs. afr.LD, pointing to a weaker drop of z-scores in the latter
242 compared to the former.

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244 As reflected in z-score profiles (Figure 3), the concordance between TADs or isochores and
245 LD-blocks, although weaker in strength (~50% drop in z-score compared to the reference ,
246 see arrows in figure 3), is evidenced by the peaked z-score profiles in all comparisons which
247 suggests that the LD-blocks tend to overlap or match TADs and isochores.

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DISCUSSION

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Interphase-leptotene chromatin reorganization

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Leptotene chromatin domains are seen as linear arrays of chromatin loops, connected

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by the synaptonemal axis, quite different from the interphase chromatin, where about 40% of

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the genome is made up of LADs. Can the pre-existing higher order chromatin structure in the

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interphase of PCG or PLS be related to those of early leptotene? As suggested by Figure 1a,

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the spatial correlation between recombination and loop structure of spermatids and ES cells

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appears to argue in favour of this link. This is consistent with the lower size of the loops

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attached to the SC in the telomeric and subtelomeric regions of mouse (Heng *et al.* 1996),

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known to be GC and gene-rich (Saccone *et al.* 1992), and with the observation that the yeast

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transcriptional landscape during meiosis dictates the preferred attachment sites of the SC axial

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elements (Sun *et al.* 2015). A parsimonious explanation could be that the chromatin loops of

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many leptotene chromosomes are, in part, inherited from the interphase of PGC or PLS

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through DNA composition constraints and active (*e.g.* H3K4me3, H3K9ac and H3K4me2)

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and/or repressive (*e.g.* H3K9me3, H3K27me3, H3K9me2) chromatin marks (Tang *et al.*

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2016, for a review). The latter could maintain these regions in a “poised” folding state and

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may happen with the contribution of protein complexes still attached to the LADs DNA

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released from the nuclear membrane (*e.g.* H3K27me3, H3K9me2), and participating later in

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the build up of chromosome axis and loops. The majority of recombination cold spots are in

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constitutive LADs (the GC-poorest isochores), which are enriched for structural variations, in

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particular deletions (Jabbari and Nürnberg 2016; Morgan *et al.* 2017), that can locally

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suppress recombination due to local homologous chromosomes miss-alignments disrupting

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synapsis (Morgan *et al.* 2017). Interestingly, artificial tethering of DSB sites to the nuclear

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lamina causes a shift from repair by homologous recombination to repair by non-homologous

273 end-joining (Lemaitre *et al.* 2014). As a consequence, lesions in GC-poor TADs and loops,
274 characterized by lower recombination, may not depend on homologous recombination for
275 their repair. In this context TAD loops will be stabilized as in mitotic chromosomes, by the
276 dynamic binding of cohesin and meiotic insulators. Since BORIS (or CTCF-like), a genomic
277 neighbour of Spo11 (Jabbari *et al.* 2018), is present in male germ cells during and after
278 meiosis, it was proposed that it may interact with at least one of the meiosis-specific subunits
279 of cohesin complexes to contribute to a progressive re-establishment of genome architecture
280 in haploid post-meiotic round spermatids (Lobanenkov *et al.* 2017).

281 The trade-off between physico-chemical constraints at the DNA level and protein
282 binding partners is expected to affect the conformation of the chromatin fibre that is believed
283 to be primarily determined by its own stiffness, which favours or restricts the formation of
284 long-range contacts (Kleckner 2006). Equally interesting in this regards are the compositional
285 constraints that shape DNA bendability (Vinogradov 2003, 2017) and super-coiling
286 (Naughton *et al.* 2013).

287

288 **LD-blocks and chromatin neighbourhoods**

289 The relative concordance between TADs or isochores and recombination or LD-
290 blocks revealed in this work has two consequences; (1) it suggests that regional variation of
291 recombination is topologically defined in concert with an underlying compositional and
292 epigenetic framework. GC-rich domains (isochores) are recombinogenic, which may explain
293 the small size of GC-rich LD-blocks and TADs sizes (Figure S3). As a result, conserved LD-
294 blocks, namely those that are shared between Europeans, east Asians and Africans, are
295 significantly larger in size (Figure S4) and their lower recombination rate is in agreement with
296 the strong LD blocks being CG-poor (Smith *et al.* 2005) and enriched in cold spots as shown
297 in figure 1a and b; (2) strong LD between a pair of SNPs in GC-rich recombinogenic TADs
298 may hint to functional chromatin contacts maintained by purifying selection. The ability of
299 LD-blocks to encompass long range SNP interactions in regions with enhanced intra-loop
300 contacts, highlights how allelic chromatin topology analyses can help to infer mechanisms by
301 which SNPs associate with disease and traits (Tang *et al.* 2015).

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303 **The Loop organization of the chromatin imposes structural constraints on**
304 **recombination**

305 It was previously anticipated that meiotic prophase has evolved directly from the latter
306 stages of the mitotic program (Kleckner 2006). This raises the possibility that when the LADs
307 disassemble (likely forming larger contact domains) and chromosomes undergo structural
308 reorganization into linear arrays of chromatin loops, the pre-existing radial loop configuration
309 keeps its “genomic footprints” on the chromatin loop/axis before the recombination process is
310 initiated. Because GC-poor TADs/LD-blocks are longer and gene poor (richer in genes with
311 large introns), one may conclude that the loops emerging from the synaptonemal complex are

312 of different sizes and may be influenced by chromatin packing within loops, leading to
313 different loop lengths (Zickler and Kleckner 1999).

314 Nucleosome formation generally restricts the accessibility of proteins to DNA,
315 including Spo11. Meiotic DSBs are reportedly introduced on the chromatin loop regions
316 that transiently interact with the lateral elements of the synaptonemal complex (Blat et al.
317 2002; Aquaviva et al. 2013; Panizza et al. 2013), suggesting that these chromatin regions
318 may contain nucleosome-depleted regions (GC-rich open chromatin) (Getun et al. 2010;
319 Kobayashi et al. 2016; Grey et al. 2017; Yamada et al. 2017). Thus, the local effect is
320 expected to be stronger in GC-rich TADs, where loops are shorter (Jabbari and Bernardi,
321 2017), nucleosomes are spaced and PRDM9 and CTCF binding sites are enriched (Grey et
322 al. 2017).

323

324 **Evolutionary considerations**

325 As mentioned in the Introduction, whether recombination determines GC level or
326 whether sequence composition drives recombination is still an open question. Because
327 CpG methylation is lower and CpG shortage is stronger in amniotes than in amphibia or
328 fishes (Jabbari et al. 1997), some authors speculated (Belle et al. 2004) that a GC-bias in
329 mismatch repair increased in the ancestor of amniotes as a consequence of an increase in
330 the level of CpG methylation. On the same basis, other authors (Fryxell and Zuckerkandl,
331 2000) hypothesized that cytosine deamination and DNA base composition affect each
332 other, generating a positive feedback loop that leads to divergent genetic drifts to high or
333 low GC%; these authors argued that cytosine deamination must be highly dependent on
334 body temperature. The body temperature hypothesis was early proposed (see Bernardi
335 2007) to explain the formation of the more stable GC-rich isochores of mammals and
336 birds. As far as the correlation between recombination and GC-TADs or isochores is
337 concerned, the GC homogeneity of fish genomes compared to mammals or birds is

338 compelling, as fish could have evolved the mammalian compositional pattern had their
339 genome evolved under BGC regimen. Advances in fish and amphibian genetics and
340 genomics will help to understand which factors could have shaped the biased substitution
341 patterns leading to the current mammalian and avian GC landscapes. Recombination COs
342 and BGC frequencies can also be influenced by environmental and physiological
343 conditions, a well-documented case is the heat-sensitivity of the chromatin axis during
344 meiosis (Morgan CH. *et al.* 2017; Lloyd *et al.* 2017). This leaves space for an interplay
345 between selection and recombination in shaping vertebrate genome organization and
346 nuclear architecture. Conservation of the correlation between recombination rates and
347 GC% in human and mouse very likely reflects the evolutionary conservation of
348 mammalian isochores and TADs (Rao *et al.* 2014; Vietri-Rudan 2015 *et al.* 2015; Jabbari
349 and Bernardi 2017). Therefore, the recombination landscape must be related to the co-
350 regulation of gene expression or insulated interactions in which chromatin folding (loops
351 and TADs) plays a critical role.

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CONCLUSIONS

354 The frequency of cold and hot spots of recombination and its relation to open chromatin
355 was suspected many decades ago, and largely confirmed later (see introduction and
356 Morgan *et al.* 2017). The recent observation of the correspondence between isochores and
357 TADs (Jabbari and Bernardi 2017) and the large number of available genomic maps
358 allowed us to observe that LD-blocks significantly, albeit weakly, match TADs and
359 isochores. Cold/hot spots of recombination are compartmentalized, they correspond to
360 AT/GC rich LADs/TADs. Binding frequencies of key determinants of meiotic
361 recombination hot spots (PRMD9, Spo11, DMC1, H3K4me3) are positively correlated
362 with TADs GC%. This implies that recombination frequency is associated with the same
363 (com)positional features that constrain the distribution of chromatin in the interphase

364 nucleus. We conclude that the chromatin loop domains in leptotene is inherited in part
365 from the chromatin conformation in interphase. The physical aggregation of cold/hot spots
366 along chromosomes, expectedly led to the finding of the LD-block/isochore/TADs
367 concordance. The recombination landscape in mammals is tied to insulated interactions in
368 which chromatin folding is crucial. Revealing a new aspect of modular recombination
369 underlying alleles co-segregation may open the way for a better understanding of the
370 mosaic architecture of genome regulation and evolution.

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